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Harding, Robert Maxwell
Becker, Douglas Keith
Hafner, Gregory John
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<120> Transcriptional Control Element, Chimeric Constructs and Uses
Therefor

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ccgaacttcc cattcttctc ttgagtcttt cctttgagct tgagcttggtg tgtaatcttt 7380
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accacacttt ttctacct 7458

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<210> 3
<211> 146
<212> PRT
<213> Taro bacilliform virus

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<400> 3

Met Ala Lys Lys Phe Glu Ala Ala Ile Lys Asp Trp Tyr Asp Asn Ser
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Arg Arg Ala Asp Leu Ser Tyr Leu Asp Leu Ala Thr Thr Thr Lys Pro
20 25 30

Ser Ala Ser Gln Leu Ala His Asn Leu Gln Val Ile Phe Asp Arg Leu
35 40 45

Ser Leu His Ser Ser Val Ser Ile Lys Glu His Tyr Glu Val Val Ser
50 55 60

Lys Leu His Ser Leu Glu Lys Ser Ile Glu Glu Leu Lys Ser Glu Leu
65 70 75 80

Thr Thr Val Lys Arg Ala Leu Thr Ser Ile Gln Lys Glu Val Phe Thr
85 90 95

His Lys Pro Leu Thr Ala Gln Glu Val Gln Thr Leu Ala Gln Ser Leu
100 105 110

Ile Lys Glu Pro Lys Gln Ile Glu Gln Gln Ala Val Phe Leu Leu Lys
115 120 125

Glu Leu Lys Glu Gln Thr Ala Lys Ile Gln Ala Leu Leu His Glu Leu
130 135 140

Lys Ser
145

<210> 4

<211> 144

<212> PRT

<213> Taro bacilliform virus

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Glu Thr Lys Val Leu Gly Asp Pro Ser Val Gly Phe Ser Glu Ile Pro
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Thr Thr Ala Ile Gly Thr Ala Thr Gly Phe Ser Thr Leu Tyr Lys Gln
 35 40 45

Asn Asn Thr Ile Ile Asn Leu Leu Ile Ser Leu His Lys Lys Val Asp
 50 55 60

Ser Leu Ser Lys Lys Thr Asp Val Asp Glu Leu Ala Thr Glu Leu Ser
 65 70 75 80

Lys Leu Thr Ile Lys Asp Thr Pro Lys Val Lys Ala Lys Thr Pro Leu
 85 90 95

Tyr Val Phe Lys Ser Pro Arg Leu Ile Leu Glu Glu Glu Arg Tyr Lys
 100 105 110

Ile Gly Leu Pro Pro Thr Thr Thr Asp Trp Thr Trp Pro Val Gly His
 115 120 125

Pro Phe Ala Pro Pro Pro Lys Thr Ser Thr Lys Ala Ser Thr Ser Ser
 130 135 140

<210> 5
 <211> 1881
 <212> PRT
 <213> Taro bacilliform virus

<400> 5

Met Ser Leu Ala Val Arg Asp Arg Gly Ser Asn Pro Ser Thr Ser Ser
 1 5 10 15

Thr Val Pro Ser Gln Gln Asp Gln Ile Arg Asp Tyr Arg Asn Met Gln
 20 25 30

Arg Val Arg His Thr Ala Glu Arg Ala Ala Arg Arg Ile Phe Pro Gly
 35 40 45

Arg Phe Asn Arg Thr Leu Glu Ser Gln Ile Asn Pro Glu Ala Glu Ile
 50 55 60

Arg Leu Ser Gln Gln Arg Arg Ala Ala Met Val Pro Ala Glu Val Leu
 65 70 75 80

Tyr Asn Thr Ser Pro Ser Thr Arg Asn Gln Lys Val Tyr Gln His Tyr

85

90

95

Ser Glu Glu Arg Ile Leu Cys Thr Gly Gln Asn Gln Gln Leu Asn Leu
 100 105 110

Pro Phe Ile Asn Glu Ser Ser Tyr Arg Ala Leu Arg Glu Ser Gly Gln
 115 120 125

Gln His Leu His Ile Gly Leu Ile Met Ile Arg Val His Pro Leu His
 130 135 140

Arg Arg Asn Ala Gly Thr Thr Ala Leu Ile Val Pro Arg Asp Ile Arg
 145 150 155 160

Trp Asn Asp Asp Arg Ser Ile Ile Gly Thr Met Glu Ile Asp Leu Ser
 165 170 175

Ala Gly Ser Gln Ile Val Tyr Ile Ala Pro Asn Ile Met Leu Ser Val
 180 185 190

Glu Asp Phe Tyr Arg Asn Ile Gln Leu Ala Ile Gln Thr Gln Gly Tyr
 195 200 205

Glu Asn Trp Asn Ser Ala Glu Ser Asn Leu Leu Ile Ser Arg Ala Leu
 210 215 220

Ile Gly Arg Leu Thr Asn Asp Ser Phe Thr Gly Phe Gln Tyr Asn Ile
 225 230 235 240

Ser Asn Val Ala Glu Tyr Leu His Ser His Gly Val Gln Ala Ile Glu
 245 250 255

Gly Gln Ala His Pro Arg Thr Leu Gly Asn Arg Trp Ile Leu Gln Ala
 260 265 270

Pro Ala Pro Pro Arg Ser Leu Val Pro Gln Asn Val Glu Thr Thr Thr
 275 280 285

Leu Leu Asp Gly Asn Val Ser Ile Arg Phe Ser Asn Tyr His Gln Ala
 290 295 300

Pro Val Asn Asp Thr Gln Asp Asn Ser His Pro Asp Ile Gln Glu Asp
 305 310 315 320

Glu Asn Gln Phe Ile Gly Phe Leu Ser Asp Leu Gly Glu Glu Tyr Glu
 325 330 335

Leu Glu Tyr Pro Ser Phe Thr Pro Val His Ala Asp Glu Phe Ile Phe
 340 345 350

Ile Ile Ile Asn Gly Glu Glu Ile Pro Asp Asp Phe Val Ser Ser Phe
 355 360 365

Cys Ser Asn Phe Ser Pro Pro Pro Ile Pro Glu Pro Glu Pro Thr Ala
 370 375 380

Ile Glu Glu Thr Ala Phe Thr Leu Glu Glu Gln Phe Asn Asp Leu Asp
 385 390 395 400

Tyr Pro Thr Leu Ile Ser Met Glu Lys Gln Leu Val Gln Ser Ser Val
 405 410 415

Thr Ser Ala Tyr Asn Pro Pro Thr Glu Pro Leu Met Gly Gln Val Val
 420 425 430

Tyr Pro Pro Ala Ser Ala Pro Arg Pro Gln Ala Glu Thr Ser Ser Thr
 435 440 445

Ser Glu Arg Phe Lys Asn Phe Arg Ala Lys Pro Tyr Ser Thr Pro Thr
 450 455 460

Ile Phe Leu Pro Pro Ala Tyr Asn Gln Gln Gly Ala Ile Leu Val Leu
 465 470 475 480

Pro Asp Asp Ile Gly Leu Tyr Glu Asp Thr Ile Ser Arg Trp Glu Ser
 485 490 495

Ile Thr Leu Asn Met Met Asn Glu Lys Val Trp Pro Ser Asn Glu Ala
 500 505 510

Lys Ala Lys Tyr Met Glu Asn Leu Leu Gly Glu Met Glu Lys Lys Thr
 515 520 525

Trp Ile Gln Trp Arg Thr Thr Tyr Val Ser Glu Tyr Asp Ala Leu Val
 530 535 540

Gln Gln Ser Asp Glu Thr Gln Asn Leu Leu Ser Gln Val Arg Arg Ile
 545 550 555 560

Phe Leu Leu Gln Asp Pro Tyr Gln Gly Ser Thr Ala Glu Gln Asp Gln
 565 570 575

Ala Tyr Asn Asp Leu Glu Arg Ile Ser Cys Asp Asn Ile Lys Asp Leu
 580 585 590

Ile Pro Tyr Leu Ile Gln Phe Arg Asn Leu Ala Ala Lys Ser Gly Arg
 595 600 605

Leu Phe Leu Gly Pro Glu Leu Ser Glu Lys Leu Phe Arg Lys Met Pro
 610 615 620

Pro Leu Ile Gly Lys Glu Ile Glu Thr Ala Phe Ile Ala Lys His Gly
 625 630 635 640

Asn Ala Asn Ile Thr Val Met Pro Arg Ile His Phe Ala Tyr His Tyr
 645 650 655

Leu Ala Glu Leu Cys Lys Lys Ala Ala Leu Gln Arg Ser Leu Lys Asp
 660 665 670

Leu Ser Phe Cys Asn Gln Ile Pro Leu Pro Gly Ile Tyr Thr Lys Gly
 675 680 685

Asn Lys Lys Phe Gly Leu Arg Lys Ala Arg Thr Tyr Lys Gly Lys Pro
 690 695 700

His Pro Thr His Val Arg Val Phe Lys Lys Ala Lys Tyr Gln Arg Thr
 705 710 715 720

Lys Lys Cys Lys Cys Phe Ile Cys Gly Glu Pro Gly His Phe Ala Arg
 725 730 735

Glu Cys Thr Lys Gln Arg Gly Asn Ile Val Arg Ala Thr Val His Gln
 740 745 750

Glu Leu Ala Ile Pro Asp Asn Phe Asp Val Val Ser Val Asp Ala Asp
 755 760 765

Glu Ser Asp Ser Ser Gly Ile Tyr Ser Tyr Ser Glu Asn Glu Ala Pro
770 775 780

Leu Gln Glu Val Asn Ser Phe Ile His Asp Glu Asn Ile Phe Phe Leu
785 790 795 800

Ser Asp Ala Asp Glu Phe Glu Ser Pro Gln Gln His Leu His Glu Thr
805 810 815

Val Asn Met Leu Gln Ser Arg Ser Ala Tyr Leu Pro Gln Val Ala Val
820 825 830

Gly Glu Glu Lys Leu Asn Cys Ser His Ile Trp Leu Gln Asp Val Asp
835 840 845

Ile Pro Ser Asp Lys His Lys Cys His Thr Cys Arg Arg Asp Thr Gln
850 855 860

Lys His Tyr Arg Leu Glu Cys Gln Lys Cys Lys Phe Leu Val Cys Ser
865 870 875 880

Leu Cys Thr Ile Pro Tyr Leu Gly Ile Thr Met Gln Phe Arg Gln Lys
885 890 895

Gln Lys Ser Gln Pro Glu Asn Pro Asn Leu Val Arg Glu Leu Leu Glu
900 905 910

His Ala Ile Phe Leu Glu Glu Lys Cys Lys Asn Gln Glu Leu Leu Ser
915 920 925

Glu Thr Gln Ile Glu Arg Ile Val Ser Ser Glu Lys Gln Val Lys Phe
930 935 940

Tyr Gly Ile Leu Pro Thr Lys Lys Ser Asn Lys Ser Ala Gly Tyr Asp
945 950 955 960

Leu Gln Ser Asn Ile Asp Ile Glu Ile Pro Pro Gly Lys Cys Thr Val
965 970 975

Ile Ser Thr Gly Thr Phe Leu Gln Met Pro Asp Asn Met Tyr Gly Arg
980 985 990

Leu Val Glu Arg Thr Ser Leu Ala Ile Gln Gly Ile Thr Val Gln Gly

995					1000					1005				
Gly Val	Ile Asp	Pro Asp	Phe Thr	Gly Glu	Ile Gln	Ile Val	Leu							
1010			1015		1020									
Phe Asn	His Asn	Thr Ala	Pro Tyr	Pro Val	Lys Lys	Thr Tyr	Arg							
1025			1030		1035									
Leu Ala	Gln Ile	Ile Phe	Glu Lys	Phe Tyr	Thr Pro	Ile Phe	Ile							
1040			1045		1050									
Gln Glu	Pro Phe	Thr Ser	Thr Gln	Gln Gly	Ser Ser	Asn Phe	Gly							
1055			1060		1065									
Ser Thr	Ala Lys	Pro Leu	Gln Ile	Thr Glu	Asn Ile	Glu Val	Met							
1070			1075		1080									
Ser Glu	Thr Val	Ala Asn	Gln Val	Ala Lys	Ser Ser	Val Leu	Pro							
1085			1090		1095									
Arg Leu	Tyr Ser	Ile Gln	Ala His	Ile His	Ile Ala	Pro Asp	Ile							
1100			1105		1110									
Val Ile	Ser Thr	Thr Ala	Ile Ile	Asp Thr	Gly Ala	Thr Val	Cys							
1115			1120		1125									
Cys Ile	Ser Glu	Lys Ile	Val Pro	Glu Ala	Ala Lys	Glu Gln	Leu							
1130			1135		1140									
Asn Tyr	Lys Val	Asn Ile	Ser Gly	Ile Ser	Ser Gln	Gln Gln	Ile							
1145			1150		1155									
Gln His	Arg Leu	Lys Arg	Gly Thr	Leu Glu	Ile Ala	Ser Asn	Lys							
1160			1165		1170									
Tyr Ala	Leu Pro	Leu Cys	Tyr Ile	Ile Glu	Leu Asn	Asp Lys	Asp							
1175			1180		1185									
Asp Phe	Ser Met	Ile Leu	Gly Cys	Asn Phe	Phe Lys	His Met	Gly							
1190			1195		1200									
Gly Gly	Met Arg	Phe Glu	Gly Pro	His Val	Thr Phe	Tyr Lys	Gly							
1205			1210		1215									

Ile Thr	Thr Leu Ser Thr Ser	Tyr Ala Asn Thr Gly	Ile Asp Thr
1220	1225	1230	
Glu His	Glu Gln Ile Thr Ser	Thr Thr Ser Gln Ser	Phe Lys Glu
1235	1240	1245	
Arg Phe	Ser Pro Leu Met Asn	Glu Leu Lys Ala Ala	Gly Tyr Ile
1250	1255	1260	
Gly Glu	Asp Pro Leu Lys His	Trp Ser Lys Asn Lys	Val Thr Cys
1265	1270	1275	
Lys Leu	Asp Leu Lys Asn Thr	Glu Ile Thr Ile Gln	Asp Lys Pro
1280	1285	1290	
Leu Arg	His Ile Thr Pro Ala	Leu Glu Gln Ser Tyr	Gly Arg His
1295	1300	1305	
Val Asn	Ala Leu Leu Met Leu	Lys Val Ile Gln Pro	Ser Lys Ser
1310	1315	1320	
Arg His	Arg Thr Met Ala Phe	Leu Val Asn Ser Gly	Thr Thr Val
1325	1330	1335	
Thr Ala	Asp Gly Lys Glu Ile	Lys Gly Lys Glu Arg	Met Val Phe
1340	1345	1350	
Asn Tyr	Lys Ala Leu Asn Asp	Asn Thr Tyr Lys Asp	Gln Tyr Ser
1355	1360	1365	
Leu Pro	Asn Ile Gln Leu Ile	Leu Lys Lys Val Ile	Asn Ser Thr
1370	1375	1380	
Ile Tyr	Ser Lys Phe Asp Leu	Lys Ser Gly Phe His	Gln Val Ala
1385	1390	1395	
Met Asp	Pro Asp Ser Val Glu	Trp Thr Ala Phe Leu	Val Pro Gln
1400	1405	1410	
Gly Leu	Tyr Glu Trp Leu Ala	Met Pro Phe Gly Leu	Lys Asn Ala
1415	1420	1425	

Pro	Ala	Val	Phe	Gln	Arg	Lys	Met	Asp	Ala	Val	Phe	Lys	Gly	Cys
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1445						1450					1455			
Asn	Asn	Glu	Glu	Asp	His	Ala	Lys	His	Leu	Val	Ile	Met	Leu	Gln
1460						1465					1470			
Arg	Cys	Lys	Glu	His	Gly	Leu	Val	Leu	Ser	Pro	Thr	Lys	Met	Asn
1475						1480					1485			
Ile	Ala	Val	Arg	Glu	Val	Asn	Phe	Leu	Gly	Ala	Thr	Ile	Gly	Ser
1490						1495					1500			
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1505						1510					1515			
Phe	Asp	Thr	Glu	Lys	Leu	Gln	Ser	Lys	Lys	Gly	Leu	Arg	Ser	Phe
1520						1525					1530			
Leu	Gly	Ile	Leu	Asn	Tyr	Ala	Arg	Asn	His	Ile	Pro	Asn	Leu	Gly
1535						1540					1545			
Lys	Ile	Ala	Gly	Pro	Leu	Tyr	Ser	Lys	Thr	Ser	Ile	Tyr	Gly	Asp
1550						1555					1560			
Ile	Arg	Phe	Ser	Ala	Ser	Asp	Trp	Lys	Leu	Ile	Asn	Glu	Ile	Lys
1565						1570					1575			
Ala	Ile	Val	Glu	Lys	Leu	Pro	Pro	Leu	Asp	Tyr	Pro	Pro	Glu	Gln
1580						1585					1590			
Ala	Tyr	Ile	Ile	Ile	Glu	Ser	Asp	Gly	Cys	Met	Glu	Gly	Trp	Gly
1595						1600					1605			
Ala	Ile	Cys	Lys	Trp	Lys	Leu	Ala	Glu	Tyr	Asp	Pro	Lys	Ser	Ser
1610						1615					1620			
Glu	Gln	Ile	Cys	Ala	Tyr	Ala	Ser	Gly	Lys	Phe	Ser	Pro	Ile	Lys
1625						1630					1635			

Ser Thr	Ile Asp Ala Glu Ile	Thr Ala Ala Met Glu	Gly Leu Glu
1640	1645	1650	
Ala Phe	Lys Ile His Tyr Leu	Asp Lys Gln Lys Ile	Thr Leu Arg
1655	1660	1665	
Thr Asp	Cys Gln Ala Ile Ile	Ser Phe Cys Asn Lys	Thr Ser Val
1670	1675	1680	
Asn Lys	Pro Ser Arg Val Arg	Trp Leu Lys Phe Ile	Asp Tyr Ile
1685	1690	1695	
Thr Asn	Thr Gly Ile Asp Val	Lys Phe Glu His Ile	Asp Ala Lys
1700	1705	1710	
Asn Asn	Val Leu Ala Asp Thr	Leu Ser Arg Leu Val	Asn Thr Leu
1715	1720	1725	
Gln Asp	Leu Pro Trp Leu Asp	Glu Pro His Gln Asp	Gln Thr Val
1730	1735	1740	
Ser Leu	Met Gln Glu Ile Glu	Asp Ala Pro Leu Glu	Ile Lys Gln
1745	1750	1755	
Arg Ser	Leu Thr Cys Leu Gln	Arg Leu Ile Cys Arg	Ser Phe Met
1760	1765	1770	
Glu Asp	Ser Thr Glu Glu Ala	Ile His Phe Leu Glu	Asp Asp Lys
1775	1780	1785	
Ile Glu	Pro Thr Ala Glu Ser	Ser Thr Pro Ile Thr	Leu Asp Glu
1790	1795	1800	
Phe Ser	Arg Lys Arg Phe Gln	Glu His Thr Asp Leu	Leu Glu Glu
1805	1810	1815	
Phe Gln	Leu Thr Leu Leu Gln	Ile Asn Leu Leu Glu	Ala Ser Leu
1820	1825	1830	
His Glu	Arg Leu Met Lys Cys	Gln Ser Tyr Ala Thr	Arg Asp Asn
1835	1840	1845	
Phe Trp	Gly Asp Trp Leu Pro	Glu Ala Arg Arg Asp	Leu Leu Gln

1850	1855	1860	
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1865	1870	1875	
His Ser Ile			
1880			
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<212>	DNA		
<213>	Taro bacilliform virus		
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taacactttg caggattttgc catggctaga tgaacctcat caggatcaaa cagtctccct			180
gatgcaggaa attgaagatg cacctcttga aatcaagcag cgttctttta cctgcttaca			240
gagactgatc tgtagaagct tcatggaaga ttctacagaa gaagctattc acttcctcga			300
agatgataag atcgagccaa cagctgagtc atcaacccca attactttgg atgaattttc			360
aagaaaaaga ttccaagaac atacagatct cttagaagaa tttcaattaa ctttgcttca			420
aattaatctt cttgaagcat ctcttcatga acgattaatg aaatgccaaa gttatgcaac			480
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ctttgtgtgt gagtggcgca cttgcgcata atgtagtaag gaattattgt acttttacgc			660
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ggggagccgt tcgtacaaag tagatgcttt tctagtcaca tctgactttt ctaaaagcag			780
atgccatcaa ctttattcga gttgagcctc ggggagccgc tcgttttaaag atgctctttt			840
gaaaatgaca gcgcgtggtg cgatgtcatt ctcacctttt ctttaatgcg tcggccaccg			900
actgcattat tgagattctc ttatcccttt gccacctcat cggttgcatt attgggattt			960
cgtatcgagt cgagggacga ggcctccact actcctataa aaggacctca acccctcaga			1020
agaacggcaa gccggaaaca ccgaacttcc cattcttctc ttgagtcttt cctttgagct			1080
tgagcttggtg tgtaatcttt catagtttct aagtctccga agaacgagca ccgtctcgtg			1140
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<210> 7
 <211> 598
 <212> DNA
 <213> Taro bacilliform virus

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 tgagcctcgg ggagccgttc gtacaaagta gatgcttttc tagtcacatc tgacttttct 180
 aaaagcagat gccatcaact ttattcgagt tgagcctcgg ggagccgctc gtttaaagat 240
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 ggccaccgac tgcattattg agattctctt atccctttgc cacctcatcg gttgcattat 360
 tgggatttcg tatcgagtcg agggacgagg cctccactac tcctataaaa ggacctcaac 420
 ccctcagaag aacggcaagc cggaaacacc gaacttccca ttcttctctt gagtctttcc 480
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 <211> 529
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 tgccatcaac tttattcgag ttgagcctcg gggagccgct cgtttaaaga tgctcttttg 180
 aaaatgacag cgcgtggtgc gatgtcattc tcaccttttc tttaatgcgt cggccaccga 240
 ctgcattatt gagattctct tatccctttg ccacctcatc ggttgcatta ttgggatttc 300
 gtatcgagtc gagggacgag gcctccacta ctccataaaa aggacctcaa cccctcagaa 360
 gaacggcaag ccggaaacac cgaacttccc attcttctct tgagtctttc ctttgagctt 420
 gagcttgtgt gtaatctttc atagtttcta agtctccgaa gaacgagcac cgtctcgtga 480
 aggagccgat ctttttccaa ccacactttt tctaccttgg tatcagagc 529

<210> 9
 <211> 261
 <212> DNA
 <213> Taro bacilliform virus

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 tactcctata aaaggacctc aaccctcag aagaacggca agccggaaac accgaacttc 120
 ccattcttct cttgagtctt tcctttgagc ttgagcttgt gtgtaatctt tcatagtttc 180
 taagtctccg aagaacgagc accgtctcgt gaaggagccg atccttttcc aaccacactt 240
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<210> 10
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Badna FP primer

<220>
 <221> modified_base
 <222> (5)..(6)
 <223> I

<220>
 <221> modified_base
 <222> (10)..(11)
 <223> I

<220>
 <221> modified_base
 <222> (18)..(19)
 <223> I

<400> 10
 atgccttygg aaraaygccc 20

<210> 11
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Badna RP primer

<220>
 <221> modified_base
 <222> (9)..(10)
 <223> I

<220>
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<222> (11)..(12)
 <223> I

<220>
 <221> modified_base
 <222> (13)..(14)
 <223> I

<220>
 <221> modified_base
 <222> (18)..(19)
 <223> I

<400> 11
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<210> 12
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 1F primer

<400> 12
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<210> 13
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> TRBR primer

<400> 13
 ctgcaggcgg ccgcgctctg atacca 26

<210> 14
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 5F primer

<400> 14
 agtcttttct ttgagcttga gc 22

<210> 15
 <211> 25
 <212> DNA

<213> Artificial Sequence
 <220>
 <223> G2R primer
 <400> 15
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 <210> 16
 <211> 12
 <212> DNA
 <213> Artificial Sequence
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 <223> Cytoplasmic initiator methionine tRNA (tRNA^{met}) binding site
 <400> 16
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 <210> 17
 <211> 25
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> F-GTN primer
 <400> 17
 ctgcagatag gattctttgt gtgtg 25
 <210> 18
 <211> 24
 <212> DNA
 <213> Artificial Sequence
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 <223> R-GTN primer
 <400> 18
 ccatgggctc tgataccaag gtag 24
 <210> 19
 <211> 20
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 <213> Artificial Sequence
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 <223> P527-F primer
 <400> 19
 ctgcagggac gccactaggc 20

<210> 20
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 <212> DNA
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 <220>
 <223> P257-F primer

 <400> 20
 ctgcaggcca cctcatcggt tgc 23

 <210> 21
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 <220>
 <223> P114-F primer

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12

27